SEQUENCE LISTING

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      LAM, TOONG JIN
      XU, YANFEI
      YAN, TIE

<120> CHIMERIC GENE CONSTRUCTS FOR GENERATION OF FLUORESCENT
      TRANSGENIC ORNAMENTAL FISH

<130> GLOF:007USC1

<140> 10/605,708
<141> 2003-10-21

<150> 09/913,898
<151> 2001-10-03

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<170> PatentIn Ver. 2.1

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                                 Met Ser Thr Arg Ser Ile Ser Tyr
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tcc agc ggt ggc tcc atc agg agg ggc tac acc agc cag tca gcc tat   161
Ser Ser Gly Gly Ser Ile Arg Arg Gly Tyr Thr Ser Gln Ser Ala Tyr
        10   15   20

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gca gta cct gcc ggc tct acc agg atg agc tca gtg acc agt gtc agg    209
Ala Val Pro Ala Gly Ser Thr Arg Met Ser Ser Val Thr Ser Val Arg
 25                  30                  35                      40

aga tct ggt gtg ggt gcc agc cca ggc ttc ggt gcc ggt ggc agc tac    257
Arg Ser Gly Val Gly Ala Ser Pro Gly Phe Gly Ala Gly Gly Ser Tyr
                     45                  50                  55

agc ttt agc agc agc agc atg ggt gga ggc tat gga agt ggt ctt ggt    305
Ser Phe Ser Ser Ser Ser Met Gly Gly Gly Tyr Gly Ser Gly Leu Gly
                 60                  65                  70

gga ggt ctc ggt ggg ggc atg ggc ttt cgt tgc ggg ctt cct atc aca    353
Gly Gly Leu Gly Gly Gly Met Gly Phe Arg Cys Gly Leu Pro Ile Thr
             75                  80                  85

gct gta act gtc aac cag aac ctg ttg gcc ccc tta aac ctg gaa atc    401
Ala Val Thr Val Asn Gln Asn Leu Leu Ala Pro Leu Asn Leu Glu Ile
         90                  95                  100

gac ccc aca att caa gct gtc cgc act tca gag aaa gag cag att aag    449
Asp Pro Thr Ile Gln Ala Val Arg Thr Ser Glu Lys Glu Gln Ile Lys
105                  110                  115                  120

acc ttc aac aac cgc ttc gct ttc ctc atc gac aaa gtg cgc ttc ctg    497
Thr Phe Asn Asn Arg Phe Ala Phe Leu Ile Asp Lys Val Arg Phe Leu
                 125                  130                  135

gaa cag cag aac aag atg ctt gag acc aaa tgg agt ctt ctc caa gaa    545
Glu Gln Gln Asn Lys Met Leu Glu Thr Lys Trp Ser Leu Leu Gln Glu
                 140                  145                  150

cag aca acc aca cgt tcc aac atc gat gcc atg ttt gag gca tac atc    593
Gln Thr Thr Thr Arg Ser Asn Ile Asp Ala Met Phe Glu Ala Tyr Ile
             155                  160                  165

tct aac ctg cgc aga cag ctc gat gga ctg gga aat gag aag atg aag    641
Ser Asn Leu Arg Arg Gln Leu Asp Gly Leu Gly Asn Glu Lys Met Lys
         170                  175                  180

ctg gag gga gag ctg aag aac atg cag ggc ctg gtt gag gac ttc aag    689
Leu Glu Gly Glu Leu Lys Asn Met Gln Gly Leu Val Glu Asp Phe Lys
105                  190                  195                  200

aac aag tac gag gat gag atc aac aag cgt gct tcc gta gag aat gag    737
Asn Lys Tyr Glu Asp Glu Ile Asn Lys Arg Ala Ser Val Glu Asn Glu
                 205                  210                  215

ttt gtc ctg ctc aag aag gat gtt gat gca gcc tac atg aac aag gtt    785
Phe Val Leu Leu Lys Lys Asp Val Asp Ala Ala Tyr Met Asn Lys Val
             220                  225                  230

gag ctt gaa gcc aag gtt gat gct ctt cag gat gag atc aac ttc ctc    833
Glu Leu Glu Ala Lys Val Asp Ala Leu Gln Asp Glu Ile Asn Phe Leu
         235                  240                  245
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agg gca gtc tac gag gct gaa ctc cgg gag ctc cag tct cag atc aag    881
Arg Ala Val Tyr Glu Ala Glu Leu Arg Glu Leu Gln Ser Gln Ile Lys
    250             255             260

gac aca tct gtt gtt gta gaa atg gac aac agc aga aac ctg gat atg    929
Asp Thr Ser Val Val Val Glu Met Asp Asn Ser Arg Asn Leu Asp Met
265             270             275             280

gac tcc atc gtg gct gaa gtt cgc gct cag tat gaa gac atc gcc aac    977
Asp Ser Ile Val Ala Glu Val Arg Ala Gln Tyr Glu Asp Ile Ala Asn
            285             290             295

cgc agc cgt gcc gag gca gag agc tgg tac aaa cag aag ttt gag gag    1025
Arg Ser Arg Ala Glu Ala Glu Ser Trp Tyr Lys Gln Lys Phe Glu Glu
            300             305             310

atg cag agc acc gct ggt cag tat ggt gat gac ctc cgc tca aca aag    1073
Met Gln Ser Thr Ala Gly Gln Tyr Gly Asp Asp Leu Arg Ser Thr Lys
            315             320             325

gct gag att gct gaa ctc aac cgc atg atc gcc cgc ctg cag aac gag    1121
Ala Glu Ile Ala Glu Leu Asn Arg Met Ile Ala Arg Leu Gln Asn Glu
    330             335             340

atc gat gct gtc aag gca cag cgt gcc aac ttg gag gct cag att gct    1169
Ile Asp Ala Val Lys Ala Gln Arg Ala Asn Leu Glu Ala Gln Ile Ala
345             350             355             360

gag gct gaa gag cgt gga gag ctg gca gtg aag gat gcc aag ctc cgc    1217
Glu Ala Glu Glu Arg Gly Glu Leu Ala Val Lys Asp Ala Lys Leu Arg
            365             370             375

atc agg gag ctg gag gaa gct ctt cag agg gcc aag caa gac atg gcc    1265
Ile Arg Glu Leu Glu Glu Ala Leu Gln Arg Ala Lys Gln Asp Met Ala
            380             385             390

cgc cag gtc cgc gag tac cag gag ctc atg aac gtc aaa ttg gct ctg    1313
Arg Gln Val Arg Glu Tyr Gln Glu Leu Met Asn Val Lys Leu Ala Leu
            395             400             405

gac att gag atc gcc acc tac agg aaa ctg ttg gaa gga gag gag agc    1361
Asp Ile Glu Ile Ala Thr Tyr Arg Lys Leu Leu Glu Gly Glu Glu Ser
    410             415             420

aga ctg tcc agc ggt gga gct caa gct acc att cat gtt cag cag acc    1409
Arg Leu Ser Ser Gly Gly Ala Gln Ala Thr Ile His Val Gln Gln Thr
425             430             435             440

tcc gga ggt gtt tca tct ggt tat ggt ggt agc ggc tct ggt ttc ggc    1457
Ser Gly Gly Val Ser Ser Gly Tyr Gly Gly Ser Gly Ser Gly Phe Gly
            445             450             455

tac agc agt ggc ttc agc agt ggt ggg tca gga tac ggt agt gga tca    1505
Tyr Ser Ser Gly Phe Ser Ser Gly Gly Ser Gly Tyr Gly Ser Gly Ser
            460             465             470

gga ttc ggt tct gga tca ggg tat ggt gga ggc tcc atc agc aaa acc    1553
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Gly Phe Gly Ser Gly Ser Gly Tyr Gly Gly Gly Ser Ile Ser Lys Thr
        475                 480                 485

agt gtc acc acc gtc agc agt aaa cgc tat taa ggagaagccc gcccaaaccc 1606
Ser Val Thr Thr Val Ser Ser Lys Arg Tyr
    490                 495

ccagccgaca cagtttccaa ccttccttac ctgcaactag atcccttctg aaccttctta 1666

cgactcaaac catctatggt gctatatttt agccagacag ctgtcccctg ttaatgagga 1726

gatgtggacg atgatttta aagtacaaaa taagttttag attgttctgt gtgttgatgg 1786

tagttacccg tatcatgcat ctcctgtctg gtggtgtcac tgccatttta aatcatcaac 1846

ccaactacac taaaacgata ccaggaagaa tcgtgctcca agccactgaa tagtcttatt 1906

tctgcactga tatgtacagg gaaagtgaga cacatagaaa ccactgtaac ctacgtagta 1966

ctatggtttc actggatcag gggtgtgcta tacaagttcc tgaatgtctt gtttgaatgt 2026

tttgtgctgt tacaagctcc ctgctgtagt tttgctgact aatctgactt ttgtcatttt 2086

gctatggctg tcagagttgg tttacctatt ttctataaaa tgtatatggc agtcagccaa 2146

taactgatga caattgcttg tgggctacta atgtccagtt acctcacatt caagggagat 2206

ctgttacagc aaaaaacagg cacaatggga tttatgtgga ccatccctcc ttaaccttgt 2266

gtactttccg tgttggaagt ggtgactgta ctgccttaca cattcccctg tattcaactg 2326

gcttccagag catattttac atccccggtt ataaatggaa aatgcaagaa aactgaaaca 2386

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ataaatctga gaccacaaaa aaaaaaaaaa aaaa                              2480


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<213> Danio rerio


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Met Ser Ser Val Thr Ser Val Arg Arg Ser Gly Val Gly Ala Ser Pro
        35                  40                  45
Gly Phe Gly Ala Gly Gly Ser Tyr Ser Phe Ser Ser Ser Ser Met Gly
    50                  55                  60
Gly Gly Tyr Gly Ser Gly Leu Gly Gly Gly Leu Gly Gly Gly Met Gly
65                  70                  75                  80
Phe Arg Cys Gly Leu Pro Ile Thr Ala Val Thr Val Asn Gln Asn Leu
                85                  90                  95
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Leu Ala Pro Leu Asn Leu Glu Ile Asp Pro Thr Ile Gln Ala Val Arg
            100   105   110
Thr Ser Glu Lys Glu Gln Ile Lys Thr Phe Asn Asn Arg Phe Ala Phe
            115   120   125
Leu Ile Asp Lys Val Arg Phe Leu Glu Gln Gln Asn Lys Met Leu Glu
            130   135   140
Thr Lys Trp Ser Leu Leu Gln Glu Gln Thr Thr Thr Arg Ser Asn Ile
145   150   155   160
Asp Ala Met Phe Glu Ala Tyr Ile Ser Asn Leu Arg Arg Gln Leu Asp
                        165   170   175
Gly Leu Gly Asn Glu Lys Met Lys Leu Glu Gly Glu Leu Lys Asn Met
                        180   185   190
Gln Gly Leu Val Glu Asp Phe Lys Asn Lys Tyr Glu Asp Glu Ile Asn
                        195   200   205
Lys Arg Ala Ser Val Glu Asn Glu Phe Val Leu Leu Lys Lys Asp Val
            210   215   220
Asp Ala Ala Tyr Met Asn Lys Val Glu Leu Glu Ala Lys Val Asp Ala
225   230   235   240
Leu Gln Asp Glu Ile Asn Phe Leu Arg Ala Val Tyr Glu Ala Glu Leu
                        245   250   255
Arg Glu Leu Gln Ser Gln Ile Lys Asp Thr Ser Val Val Val Glu Met
            260   265   270
Asp Asn Ser Arg Asn Leu Asp Met Asp Ser Ile Val Ala Glu Val Arg
            275   280   285
Ala Gln Tyr Glu Asp Ile Ala Asn Arg Ser Arg Ala Glu Ala Glu Ser
            290   295   300
Trp Tyr Lys Gln Lys Phe Glu Glu Met Gln Ser Thr Ala Gly Gln Tyr
305   310   315   320
Gly Asp Asp Leu Arg Ser Thr Lys Ala Glu Ile Ala Glu Leu Asn Arg
                        325   330   335
Met Ile Ala Arg Leu Gln Asn Glu Ile Asp Ala Val Lys Ala Gln Arg
                        340   345   350
Ala Asn Leu Glu Ala Gln Ile Ala Glu Ala Glu Glu Arg Gly Glu Leu
            355   360   365
Ala Val Lys Asp Ala Lys Leu Arg Ile Arg Glu Leu Glu Glu Ala Leu
            370   375   380
Gln Arg Ala Lys Gln Asp Met Ala Arg Gln Val Arg Glu Tyr Gln Glu
385   390   395   400
Leu Met Asn Val Lys Leu Ala Leu Asp Ile Glu Ile Ala Thr Tyr Arg
                        405   410   415
Lys Leu Leu Glu Gly Glu Glu Ser Arg Leu Ser Ser Gly Gly Ala Gln
                        420   425   430
Ala Thr Ile His Val Gln Gln Thr Ser Gly Gly Val Ser Ser Gly Tyr
            435   440   445
Gly Gly Ser Gly Ser Gly Phe Gly Tyr Ser Ser Gly Phe Ser Ser Gly
            450   455   460
Gly Ser Gly Tyr Gly Ser Gly Ser Gly Phe Gly Ser Gly Ser Gly Tyr
465   470   475   480
Gly Gly Gly Ser Ile Ser Lys Thr Ser Val Thr Thr Val Ser Ser Lys
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Arg Tyr

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ttgtgcagtg ttagaaaccg caatc atg cct ttc gga aac acc cac aac aac   112
                            Met Pro Phe Gly Asn Thr His Asn Asn
                            1   5

ttc aag ctg aac tac tca gtt gat gag gag tat cca gac ctt agc aag   160
Phe Lys Leu Asn Tyr Ser Val Asp Glu Glu Tyr Pro Asp Leu Ser Lys
 10   15   20   25

cac aac aac cac atg gcc aag gtg ctg act aag gaa atg tat ggc aag   208
His Asn Asn His Met Ala Lys Val Leu Thr Lys Glu Met Tyr Gly Lys
                30   35   40

ctt agg gac aag cag acc cca cct gga ttc act gtg gat gat gtc atc   256
Leu Arg Asp Lys Gln Thr Pro Pro Gly Phe Thr Val Asp Asp Val Ile
                45   50   55

cag act ggt gtt gac aat cca ggc cac ccc ttc atc atg acc gtc ggc   304
Gln Thr Gly Val Asp Asn Pro Gly His Pro Phe Ile Met Thr Val Gly
            60   65   70

tgt gtt gct ggt gat gag gag tcc tac gat gtt ttc aag gac ctg ttc   352
Cys Val Ala Gly Asp Glu Glu Ser Tyr Asp Val Phe Lys Asp Leu Phe
        75   80   85

gac ccc gtc att tcc gac cgt cac ggt gga tac aag gca act gac aag   400
Asp Pro Val Ile Ser Asp Arg His Gly Gly Tyr Lys Ala Thr Asp Lys
 90   95   100   105

cac aag acc gac ctc aac ttt gag aac ctg aag ggt ggt gat gac ctg   448
His Lys Thr Asp Leu Asn Phe Glu Asn Leu Lys Gly Gly Asp Asp Leu
                110   115   120

gac ccc aac tac ttc ctg agc agc cgt gtg cgt acc gga cgc agc atc   496
Asp Pro Asn Tyr Phe Leu Ser Ser Arg Val Arg Thr Gly Arg Ser Ile
                125   130   135

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aag gga tac ccc ctg ccc ccc cac aac agc cgt gga gag cgc aga gct    544
Lys Gly Tyr Pro Leu Pro Pro His Asn Ser Arg Gly Glu Arg Arg Ala
        140             145             150

gtg gag aag ctg tct gtt gaa gct ctg agt agc ttg gat gga gag ttc    592
Val Glu Lys Leu Ser Val Glu Ala Leu Ser Ser Leu Asp Gly Glu Phe
        155             160             165

aag ggc aag tac tac ccc ctg aag tcc atg act gat gac gag cag gag    640
Lys Gly Lys Tyr Tyr Pro Leu Lys Ser Met Thr Asp Asp Glu Gln Glu
170             175             180             185

cag ctg atc gct gac cac ttc ctc ttt gac aaa ccc gtc tcc ccc ctg    688
Gln Leu Ile Ala Asp His Phe Leu Phe Asp Lys Pro Val Ser Pro Leu
                190             195             200

ctg ctg gct gct ggt atg gcc cgt gac tgg ccc gat gcc aga ggc att    736
Leu Leu Ala Ala Gly Met Ala Arg Asp Trp Pro Asp Ala Arg Gly Ile
            205             210             215

tgg cac aat gag aac aaa gcc ttc ctg gtc tgg gtg aaa cag gag gat    784
Trp His Asn Glu Asn Lys Ala Phe Leu Val Trp Val Lys Gln Glu Asp
        220             225             230

cac ctg cgt gtc att tcc atg cag aag ggt ggc aac atg aag gaa gtg    832
His Leu Arg Val Ile Ser Met Gln Lys Gly Gly Asn Met Lys Glu Val
        235             240             245

ttc aag cgc ttc tgc gtt ggt ctt cag agg att gag gaa att ttc aag    880
Phe Lys Arg Phe Cys Val Gly Leu Gln Arg Ile Glu Glu Ile Phe Lys
250             255             260             265

aag cac aac cat ggg ttc atg tgg aac gag cat ctt ggt ttc gtc ctg    928
Lys His Asn His Gly Phe Met Trp Asn Glu His Leu Gly Phe Val Leu
            270             275             280

acc tgc ccc tcc aac ctg ggc aca ggc ctg cgc ggt gga gtc cac gtc    976
Thr Cys Pro Ser Asn Leu Gly Thr Gly Leu Arg Gly Gly Val His Val
            285             290             295

aag ctg ccc aag ctc agc aca cat gcc aag ttt gag gag atc ctg acc   1024
Lys Leu Pro Lys Leu Ser Thr His Ala Lys Phe Glu Glu Ile Leu Thr
            300             305             310

aga ctg cgc ctg cag aag cgt ggc aca ggg ggt gtg gac acc gct tcc   1072
Arg Leu Arg Leu Gln Lys Arg Gly Thr Gly Gly Val Asp Thr Ala Ser
        315             320             325

gtt ggt gga gtg ttt gac att tcc aac gct gac cgt atc ggc tct tca   1120
Val Gly Gly Val Phe Asp Ile Ser Asn Ala Asp Arg Ile Gly Ser Ser
330             335             340             345

gag gtt gag cag gtg cag tgt gtg gtt gat ggt gtc aag ctg atg gtg   1168
Glu Val Glu Gln Val Gln Cys Val Val Asp Gly Val Lys Leu Met Val
            350             355             360

gag atg gag aag aag ctg gga gaa ggc cag tcc atc gac agc atg atc   1216
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Glu Met Glu Lys Lys Leu Gly Glu Gly Gln Ser Ile Asp Ser Met Ile
            365                 370                 375

cct gcc cag aag taa agcgggaggc ccttccattt ttttcttcgt ctttgtctgt    1271
Pro Ala Gln Lys
            380

ttttttacag tccaacagca acgsagagga aaactgctgc tcaaaaagac agtctcacct    1331

ttgcacctgt cttctttcct tttttttccct tcttctctaa tttccatgtc atttcgccat    1391

cttttttttcc actttgtttc ctattaagtc ggtaacatct tgggatcaga tacccggsgc    1451

aggagtgagt gcttgttgct gaggcttcac ctcaatttca gccttggttg taaaaagtga    1511

atcaatcaaa gttgtatttc aaaataaaaa tccccaataa aaaaaaaaaa aaaaaaaaaa    1571

aaaaaaaaaa aaaaaaa                                                    1589


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            20                  25                  30
Val Leu Thr Lys Glu Met Tyr Gly Lys Leu Arg Asp Lys Gln Thr Pro
            35                  40                  45
Pro Gly Phe Thr Val Asp Asp Val Ile Gln Thr Gly Val Asp Asn Pro
        50                  55                  60
Gly His Pro Phe Ile Met Thr Val Gly Cys Val Ala Gly Asp Glu Glu
 65                  70                  75                  80
Ser Tyr Asp Val Phe Lys Asp Leu Phe Asp Pro Val Ile Ser Asp Arg
                85                  90                  95
His Gly Gly Tyr Lys Ala Thr Asp Lys His Lys Thr Asp Leu Asn Phe
            100                 105                 110
Glu Asn Leu Lys Gly Gly Asp Asp Leu Asp Pro Asn Tyr Phe Leu Ser
            115                 120                 125
Ser Arg Val Arg Thr Gly Arg Ser Ile Lys Gly Tyr Pro Leu Pro Pro
        130                 135                 140
His Asn Ser Arg Gly Glu Arg Arg Ala Val Glu Lys Leu Ser Val Glu
145                 150                 155                 160
Ala Leu Ser Ser Leu Asp Gly Glu Phe Lys Gly Lys Tyr Tyr Pro Leu
                165                 170                 175
Lys Ser Met Thr Asp Asp Glu Gln Glu Gln Leu Ile Ala Asp His Phe
            180                 185                 190
Leu Phe Asp Lys Pro Val Ser Pro Leu Leu Leu Ala Ala Gly Met Ala
            195                 200                 205
Arg Asp Trp Pro Asp Ala Arg Gly Ile Trp His Asn Glu Asn Lys Ala
        210                 215                 220
Phe Leu Val Trp Val Lys Gln Glu Asp His Leu Arg Val Ile Ser Met
225                 230                 235                 240
Gln Lys Gly Gly Asn Met Lys Glu Val Phe Lys Arg Phe Cys Val Gly
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                    245                    250                          255
Leu Gln Arg Ile Glu Glu Ile Phe Lys Lys His Asn His Gly Phe Met
            260                    265                          270
Trp Asn Glu His Leu Gly Phe Val Leu Thr Cys Pro Ser Asn Leu Gly
        275                    280                          285
Thr Gly Leu Arg Gly Gly Val His Val Lys Leu Pro Lys Leu Ser Thr
    290                    295                          300
His Ala Lys Phe Glu Glu Ile Leu Thr Arg Leu Arg Leu Gln Lys Arg
305                    310                          315                    320
Gly Thr Gly Gly Val Asp Thr Ala Ser Val Gly Gly Val Phe Asp Ile
                325                    330                          335
Ser Asn Ala Asp Arg Ile Gly Ser Ser Glu Val Glu Gln Val Gln Cys
            340                    345                          350
Val Val Asp Gly Val Lys Leu Met Val Glu Met Glu Lys Lys Leu Gly
            355                    360                          365 ·
Glu Gly Gln Ser Ile Asp Ser Met Ile Pro Ala Gln Lys
    370                    375                          380


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               Met Pro Arg Glu Asp Arg Ala Thr Trp Lys Ser Asn
                1                 5                    10

tat ttt ctg aaa atc atc caa ctg ctg gat gac ttc ccc aag tgt ttc    158
Tyr Phe Leu Lys Ile Ile Gln Leu Leu Asp Asp Phe Pro Lys Cys Phe
        15                    20                    25

atc gtg ggc gca gac aat gtc ggc tcc aag cag atg cag acc atc cgt    206
Ile Val Gly Ala Asp Asn Val Gly Ser Lys Gln Met Gln Thr Ile Arg
    30                    35                    40
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ctg tcc ctg cgg ggc aag gcc gtc gtg ctc atg ggg aaa aac acc atg      254
Leu Ser Leu Arg Gly Lys Ala Val Val Leu Met Gly Lys Asn Thr Met
     45              50              55              60

atg agg aag gcc att cgt ggc cac ctg gaa aac aac cca gct ctg gag      302
Met Arg Lys Ala Ile Arg Gly His Leu Glu Asn Asn Pro Ala Leu Glu
                 65              70              75

agg ctg ctt ccc cac atc cgc ggg aac gtg ggc ttc gtc ttc acc aag      350
Arg Leu Leu Pro His Ile Arg Gly Asn Val Gly Phe Val Phe Thr Lys
                 80              85              90

gag gat ctg act gag gtc cga gac ctg ctg ctg gca aac aaa gtg ccc      398
Glu Asp Leu Thr Glu Val Arg Asp Leu Leu Leu Ala Asn Lys Val Pro
             95              100             105

gct gct gcc cgt gct ggt gcc atc gcc ccc tgt gag gtg act gtg ccg      446
Ala Ala Ala Arg Ala Gly Ala Ile Ala Pro Cys Glu Val Thr Val Pro
     110             115             120

gcc cag aac acc ggg ctc ggt cct gag aag acc tct ttc ttc cag gct      494
Ala Gln Asn Thr Gly Leu Gly Pro Glu Lys Thr Ser Phe Phe Gln Ala
125             130             135             140

ttg gga atc acc acc aag atc tcc aga gga acc att gaa atc ttg agt      542
Leu Gly Ile Thr Thr Lys Ile Ser Arg Gly Thr Ile Glu Ile Leu Ser
                 145             150             155

gac gtt cag ctt atc aaa cct gga gac aag gtg ggc gcc agc gag gcc      590
Asp Val Gln Leu Ile Lys Pro Gly Asp Lys Val Gly Ala Ser Glu Ala
                 160             165             170

acg ctg ctg aac atg ctg aac atg ctg aac atc tcg ccc ttc tcc tac      638
Thr Leu Leu Asn Met Leu Asn Met Leu Asn Ile Ser Pro Phe Ser Tyr
                 175             180             185

ggg ctg atc atc cag cag gtg tat gat aac ggc agt gtc tac agc ccc      686
Gly Leu Ile Ile Gln Gln Val Tyr Asp Asn Gly Ser Val Tyr Ser Pro
     190             195             200

gag gtg ctg gac atc act gag gac gcc ctg cac aag agg ttc ctg aag      734
Glu Val Leu Asp Ile Thr Glu Asp Ala Leu His Lys Arg Phe Leu Lys
205             210             215             220

ggt gtg agg aac atc gcc agt gtg tgt ctg cag atc ggc tac cca act      782
Gly Val Arg Asn Ile Ala Ser Val Cys Leu Gln Ile Gly Tyr Pro Thr
                 225             230             235

ctt gct tcc atc cct cac act atc atc aat gga tac aag agg gtc ctg      830
Leu Ala Ser Ile Pro His Thr Ile Ile Asn Gly Tyr Lys Arg Val Leu
                 240             245             250

gct gtc act gtc gaa aca gac tac aca ttc ccc ttg gct gag aag gtg      878
Ala Val Thr Val Glu Thr Asp Tyr Thr Phe Pro Leu Ala Glu Lys Val
                 255             260             265

aag gcc tac ctg gct gat ccc acc gct ttc gct gtt gca gcc cct gtt      926
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Lys Ala Tyr Leu Ala Asp Pro Thr Ala Phe Ala Val Ala Ala Pro Val
    270                 275                 280

gcg gca gct aca gag cag aaa tcc gct gct cct gcg gct aaa gag gag    974
Ala Ala Ala Thr Glu Gln Lys Ser Ala Ala Pro Ala Ala Lys Glu Glu
285                 290                 295                 300

gca ccc aag gag gat tct gag gag tct gat gaa gac atg ggc ttc ggc    1022
Ala Pro Lys Glu Asp Ser Glu Glu Ser Asp Glu Asp Met Gly Phe Gly
                    305                 310                 315

ctg ttt gat taa accagacacc gaatatccat gtctgtttaa catcaataaa       1074
Leu Phe Asp
            320

acatctggaa aaaaaaaaaa aaaaaaaaaa                                   1104
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<210> 6
<211> 319
<212> PRT
<213> Danio rerio

<400> 6
Met Pro Arg Glu Asp Arg Ala Thr Trp Lys Ser Asn Tyr Phe Leu Lys
 1               5                  10                  15
Ile Ile Gln Leu Leu Asp Asp Phe Pro Lys Cys Phe Ile Val Gly Ala
            20                  25                  30
Asp Asn Val Gly Ser Lys Gln Met Gln Thr Ile Arg Leu Ser Leu Arg
            35                  40                  45
Gly Lys Ala Val Val Leu Met Gly Lys Asn Thr Met Met Arg Lys Ala
        50                  55                  60
Ile Arg Gly His Leu Glu Asn Asn Pro Ala Leu Glu Arg Leu Leu Pro
65                  70                  75                  80
His Ile Arg Gly Asn Val Gly Phe Val Phe Thr Lys Glu Asp Leu Thr
                85                  90                  95
Glu Val Arg Asp Leu Leu Leu Ala Asn Lys Val Pro Ala Ala Ala Arg
            100                 105                 110
Ala Gly Ala Ile Ala Pro Cys Glu Val Thr Val Pro Ala Gln Asn Thr
        115                 120                 125
Gly Leu Gly Pro Glu Lys Thr Ser Phe Phe Gln Ala Leu Gly Ile Thr
        130                 135                 140
Thr Lys Ile Ser Arg Gly Thr Ile Glu Ile Leu Ser Asp Val Gln Leu
145                 150                 155                 160
Ile Lys Pro Gly Asp Lys Val Gly Ala Ser Glu Ala Thr Leu Leu Asn
                165                 170                 175
Met Leu Asn Met Leu Asn Ile Ser Pro Phe Ser Tyr Gly Leu Ile Ile
                180                 185                 190
Gln Gln Val Tyr Asp Asn Gly Ser Val Tyr Ser Pro Glu Val Leu Asp
            195                 200                 205
Ile Thr Glu Asp Ala Leu His Lys Arg Phe Leu Lys Gly Val Arg Asn
        210                 215                 220
Ile Ala Ser Val Cys Leu Gln Ile Gly Tyr Pro Thr Leu Ala Ser Ile
225                 230                 235                 240
Pro His Thr Ile Ile Asn Gly Tyr Lys Arg Val Leu Ala Val Thr Val
                245                 250                 255
Glu Thr Asp Tyr Thr Phe Pro Leu Ala Glu Lys Val Lys Ala Tyr Leu
```

```
              260                   265                   270
Ala Asp Pro Thr Ala Phe Ala Val Ala Ala Pro Val Ala Ala Ala Thr
          275                   280                   285
Glu Gln Lys Ser Ala Ala Pro Ala Ala Lys Glu Glu Ala Pro Lys Glu
      290                   295                   300
Asp Ser Glu Glu Ser Asp Glu Asp Met Gly Phe Gly Leu Phe Asp
305                   310                   315
```

```
<210> 7
<211> 2241
<212> DNA
<213> Danio rerio

<220>
<221> TATA signal
<222> (2103)..(2108)

<220>
<221> primer bind
<222> (2221)_.(2241)
<223> CK2

<220>
<221> misc feature
<222> (2142)..(2235)
<223> Identical to the 5' CK cDNA

<400> 7
ccttcccttc tacttttgac gtccttttaa gattactcat ctcaaacacc catacaaagg 60
tcacacctgg tttatactat gatagttgta cagtgctggc tgtgacaccc aactgctgcc 120
aattgtctga ctatgcaggg tgtctatgcg tatagtttac agttagacca aagtgtgctg 180
gtgtgtgaag taacaaatga caaatactca aattgtaatt tactaagtag tttaaaaatg 240
tagtgcagtg ttggtacttt tatttcactt ttattcttgt ctatgtggat tagacaaatc 300
acatagaagg taaatcacat cataatgaac agcaaactgt ttgccagcat taaaagaaga 360
agactgctta gatgcatgtc actgatgaga aaataacttt aaacgcacac aagacggcac 420
gtaccccaac gcagtgggga cgttgcattt gaactcaacg tcaggtcgat gtcaatgttc 480
ctaatgatgt tacagcttga tgttatgcgg ggattatggt tgccatacct gatgaataaa 540
ggttcgacat tggattttgg tcgctttcca cctatgacat cgttattgga cgtcaaaata 600
aatttaggtc accacaacct atatttaacc tgctgggcaa taactaaatg cactacagaa 660
taaatgcatc agcttttcac agcataatac aaaagctact tttcactcat actttgagta 720
acatttttag gcatgtattg atatttttac cagccctccc catacataat cgtatgttta 780
acattagctt tgttagccgc tagcattact gagcttgtgc atgaaagcag atttggagct 840
gatgattgcc gtaccatgat ctcacacctt gacgattgcg taatgctatt aaatgcccat 900
atttcgtgtt gacttgcacg agaaatgaga tgggaacatt tatcagtggt cattaaatac 960
tatttttgtg ttagcttagc tgcagttttt aactattgta attaagtagt ttttctcaga 1020
tgtacttttta ctttcccttg agtacatttt ccttccttca acctgcagtc actactttat 1080
agtcctgtga ttcctgtcca atcaaattgc taccttaaga catgggccat ttataattgc 1140
tgtcaaaaat atttacacgc attaacccag agatgatgga tgtttactgt atgatgaccg 1200
aagacgtcaa catggcgtta ggttgacgtt gtttagaaa tgaaaattag gttgacgtca 1260
aacatccaat ctaaaatcat atatcaatgt atgttacccc tatgacgtct atcagacgtt 1320
tgtcattatt tgacgttggt ttaagatgtt acacaaccta atccaccaa atattaactt 1380
acaatatcct tagatgctgg ctagactttg taatattaac atcttatgat gttgtgtgcc 1440
tgttacgttt acacacatgt aaattacatg tcactactta ctactcttga gtactttaa 1500
atatttacaa ctgatacttt tactcgcact tatgattttt cagtactctt tccactactg 1560
cacatatggt ggagtttaga gccataatct gtgcagaatt gtgtgtgtgc acattttcca 1620
atatcaatac agaaggaaac tgtgttccct gttcccttgt aaatctcaac aatgcaactg 1680
```

```
ttcagctcag ggggaaaaat gccctgccag atccaaacgg ctggcaaaag tgaatggaaa 1740
aaagcctttc attaatgtga aagttgctgc gcgccccacc cagataaaaa·gagcagaggt 1800
taacatgctc tctacggctg tccagccaac cagatactga ggcagaaaca cacccgctgg 1860
cagatggtga gagctacact gtcttttcca gagtttctac tggaatgcct gtcctcaagt 1920
ctcaagcctc tccttgcatt ctctcattcc acctggggca aagccccagg ctgggtgtga 1980
caacatttat cttaccactt tctctctgta cctgtctaac aggtagggtg tgtgtgagag 2040
tgcgtatgtg tgcaagtgcg tgtgtgtgtg agagcagtca gctccaccct ctcaagagtg 2100
tgtataaaat tggtcagcca gctgctgaga gacacgcaga gggactttga ctctcctttg 2160
tgagcaacct cctccactca ctcctctctc agagagcact ctcgtacctc cttctcagca 2220
actcaaagac acaggatccg g                                         2241

<210> 8
<211> 1456
<212> DNA
<213> Danio rerio

<220>
<221> TATA signal
<222> (1389)..(1394)

<220>
<221> primer bind
<222> (1433)_.(1456)
<223> MCK2

<220>
<221> misc feature
<222> (1428)..(1453)
<223> Identical to the 5' MCK cDNA

<400> 8
gaattgcaaa gtcagagtaa taaaatgaaa ccaaaaaaca tttttaaata tacttgtctc 60
tgtggcttaa tcttggctga tgtgtgtgtg tgtgtgtgtg tacttgacag ctgctagtga 120
gcatgtgcac catgacaggc ctgttattca cacttggtgc catgttggag actgttcggc 180
cagctatagt tttcttcaca gagtcctggg tcacctaatg tcacaaggaa gaaacatgtt 240
acatgttaaa atgtgacatt caaattgtag tgcattactt aacgaaacgc attacacaag 300
ttacagctta aaagattgct agacagaaaa accagggagg ggttttccca taatatccag 360
tgagactcta ggagcgggaa cactaacagg cctccctgag tgagaacatt gcatgtgcgc 420
gtgacagaaa accagagatg gaaatacctt cttttgaatt gcataattgc ttaaaagaag 480
acacaacagg gatagttcac ccaaaaaaca gaccattctt tttttctgtt gaacaaaaat 540
taagatattt tgaagaatgc ttaccgaata acttccatat ttggaaacta attacagtga 600
aagtcaatgg gtcttccagc atttttcaa tataccttac tttgagttca aaagaaaaac 660
acatctcaaa taggtttgag gttgaataaa catttttcat tttggggtgg actatcccta 720
attatttgac acttaagatt tatagtaaat cattttatag actttctccc cttattaaac 780
atggttgaat ttatcttcat gtttatgtct gggttgtgct tttttgaaaa gatttccctg 840
tcaaatgttt ttgtgtatgg ttggcgcaca atagactgaa ctggcctatc acacagactt 900
tcataacaac tccagttgat gccctttcac cctcagtgta aaatatggc gtctgacatg 960
agcagattaa acacgacact gcaacaactt tacctgtaaa aatacaaatt gagtttgcac 1020
ccagaatcat gtggtgaacg aagcctacca agagattttt gaaagccatc ggcctgacac 1080
gcgcacttct gatatctgtg gtatgtttgg caaaagtgct gctcagcctt tttagcatgg 1140
cagatcctcc acatcccatc acccctcctt caacctattc cctcctggaa agctatgtat 1200
ggggcgggaa gtgtaaatgg atatgggaag gaaggggggc accacccaca gctgccacct 1260
catctaggat gcctggggcc taaattgaag cctttcttac actaaacagg gcataagaga 1320
ccagcgccag ccaatcataa ttcagtgagc tctaaaatgg gccagccaat ggctgcaggg 1380
gctagaggta tatatatcca aatcaaactc ttcttgcttg ggtgacccct atttcggctt 1440
ggtgaacagg atccgg                                               1456
```

<210> 9
<211> 2205
<212> DNA
<213> Danio rerio

<220>
<221> primer bind
<222> (2179)..(2205)
<223> ARP2

<220>
<221> misc_feature
<222> (2153)..(2199)
<223> Identical to the 5' ARP cDNA

<220>
<221> intron
<222> (792)..(2152)

<220>
<221> misc_feature
<222> (775)..(791)
<223> Identical to the 5' ARP cDNA

<400> 9
```
atctgtatta agaaacactt aaaatatata tgcgttacga attaaaaaca aaacacgatc  60
attttaattt gtgttgtata attttacatt ttgtaagtat tatttttata aaaaatatat 120
agaaataata caaatttgtt tacagtattc ttagttattg caataaacga attttatata 180
gaaagagaaa gagtttttatt ataagatgtt caatttaaaa aatggcagaa aatagaaaaa 240
tgattgtcaa gatgataaaa gtcagtttag acaaaaaaat aagatgaaaa acatcaaaat 300
agataataaa gtgacttttt tgggcggacc aaatttccct attaatggtc aattcattaa 360
aatacattca ttaaaataaa ggtattgcga tgaatttaga tgcacagtga ttttggttct 420
gtgcagattt ttggctgttg ttagaaggga tacatctgcg gccgaaagtt aacgggaact 480
atttacattc tttgctatta aattatccat tatttgtatt ttattacccc aaccgtaaac 540
tcaaccctca cagtaatgta aaaatattat ttattgtttt atagcgtcac agaatgatgc 600
tatattgacc gcagctgtat cctttctaag tgcgactgta caaatacgca ctgaccgtga 660
cagacacgtg cattgaccaa tcagcgcaca gatacgcatt ttccgcgcga ttctgattgg 720
atgatcgact gatactaata ttgtgccgct tcctttcgcg gcctctttct ttcacgcgtc 780
cctaccgtga ggtaaggctg acgccgctct tgtggcggtt tcttaaaatg tgttaataaa 840
taacatcata agaggtcacg agaaggtcta cgtgtgttta atatcagcgg cggttattat 900
tatgcgttta aagcttgtgt aatgattttt acagtaaaag ttagcactag cctgttagca 960
caggcctcgt gcgccatgtg tgacgcgacg ttttaatagc atcttatttg attttgatga 1020
tccgattctg atattaatca tatttatgcg taaaatgtgt gatgggtctg ctagtggaca 1080
ttacatgcta gtacttgtgc tagtcggtcg atccacattg agatgttgcg ctatttgcca 1140
ttttaaaacc agttactctc attttagtga aatattctta agccactaag ttaaaatttg 1200
tcaatcacat ataattgtgt ttatgtttta tttgagtcat cataccaggt aatagtttta 1260
tttatattag tatgtacaat ttggcataaa ctgccttcgg ttttgattga catctacttt 1320
gtaaaggtaa tcttaaaggg gtaaaggctc acccaaaaga caattcaccg tcaagtgttt 1380
tcaaatctta tgagtttctt aatgaacatg gtatgttttg gagaaaactg gaaaccaact 1440
accataatac aaatacagga aaaatatact atagaagtcg atggttacag gttttctgca 1500
ttcaaaatat ctacacaagt gtttaatgga aggaactcaa gtgatttgaa aagttaaggg 1560
tgcataaatc agttttcatt tgggtgagct gtctctaaac atttgattta gacacctcag 1620
gcagtggtca ccaagcttgt tcctgaaggg ccagtgtcct acagatttta gctccaaccc 1680
taattaaaca cacctgaaca agctaatcaa ggtcttacta ggtatgtttg aaacatccag 1740
gcaggtgtgt tgatgcaaga tagagctaaa ccctgcaggg acaatggccc aacaggattg 1800
gtgacccctg cctcaagcca tcacaaatgc attatggtat taagaaatgt gcaggttcag 1860
```

```
ttatggacag gctgttgcag tgcttgttcg tcgttcccac tgcacaaatg aacatgattc 1920
cttctatccc tgtctgtctg catctcatga cttgcaggga cgctggtctc agacacgttt 1980
atagcagtaa atcaaataca atagtgctct gattatcttt aaatatttga aagcttataa 2040
taggcaacca aattacctgg aaacagttta caaacagtaa ttcatatttt gtcatttaat 2100
aagatgcaca caaggcaggt gtaaaagtat tgcttgtgtt tgtaatcctc agatttttaca 2160
accttgtctt taaaccggct gttcaccgat ccttggaagg gatcc            2205


<210> 10
<211> 24
<212> DNA
<213> Artificial Sequence


<220>
<223> Description of Artificial Sequence: Cytokeratin - gene specific primer


<400> 10
cgctggagta agagatagac ctgg                                      24


<210> 11
<211> 26
<212> DNA
<213> Artificial Sequence


<220>
<223> Description of Artificial Sequence: Cytokeratin gene specific primer


<220>
<221> misc feature
<222> (1)..(6)
<223> Introduced for restriction site


<220>
<221> misc feature
<222> (3)..(8)
<223> BamHI site


<400> 11
ccggatcctg tgtctttgag ttgctg                                    26


<210> 12
<211> 24
<212> DNA
<213> Artificial Sequence


<220>
<223> Description of Artificial Sequence:
      Muscle creatine kinase gene specific primer


<220>
<221> misc feature
<222> (3)..(8)
<223> BamHI site


<400> 12
```

ccggatcctt gggatcagat cctg   24

<210> 13
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Muscle creatine kinase gene specific primer

<220>
<221> misc feature
<222> (1)..(3)
<223> Introduced for restriction site

<220>
<221> misc feature
<222> (3)..(B)
<223> BamHI site

<400> 13
ccggatcctg ttcaccaagc cgaa   24

<210> 14
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Acidic ribosomal protein PO gene specific primer

<400> 14
tagttggact tccacgtgcc ctgtc   25

<210> 15
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Acidic ribosomal protein PO gene specific primer

<220>
<221> misc feature
<222> (1)..(7)
<223> Introduced for restriction site

<220>
<221> misc feature
<222> (1)..(6)
<223> BamHI site

```
<400> 15
ggatcccttc caaggatcgg tgaaca                                    26


<210> 16
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide for linker used in linker-mediated PCR

<400> 16
gttcatcttt acaagctagc gctgaacaat gctgtggaca agcttgaatt c      51


<210> 17
<211> 10
<212> DNA
<213> Artificial Sequence

<223> Description of Artificial Sequence:
      Oligonucleotide for linker used in linker-mediated PCR

<220>
<221> misc_feature
<222> (10)..(10)
<223> n is a dideoxycytidine

<400> 17
gaattcaagn                                                     10


<210> 18
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      linker specific primer

<400> 18
gttcatcttt acaagctagc g                                        21


<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      linker specific primer
```

<400> 19
tcctgaacaa tgctgtggac   20

<210> 20
<211> 1392
<212> DNA
<213> Danio rerio

<220>
<221> CDS
<222> (42)..(551)

<220>
<221> primer bind
<222> (6)..(28)
<223> M2

<220>
<221> primer bind
<222> (23)..(45)
<223> M1

<220>
<221> polyA signal
<222> (797)..(802)

<220>
<221> polyA_signal <222> (1351)..(1357)

<400> 20
ctcttcttga tcttcttaga cttcacacat accgtctcga c atg gca ccc aag aag 56
                                             Met Ala Pro Lys Lys
                                               1   5

gcc aag agg agg gca gca gga gga gag ggt tcc tcc aac gtc ttc tcc 104
Ala Lys Arg Arg Ala Ala Gly Gly Glu Gly Ser Ser Asn Val Phe Ser
              10   15   20

atg ttt gag cag agc cag att cag gag tac aaa gag gct ttc aca atc 152
Met Phe Glu Gln Ser Gln Ile Gln Glu Tyr Lys Glu Ala Phe Thr Ile
          25   30   35

att gac cag aac aga gac ggt atc atc agc aaa gac gac ctt agg gac 200
Ile Asp Gln Asn Arg Asp Gly Ile Ile Ser Lys Asp Asp Leu Arg Asp
          40   45   50

gtg ttg gcc tca atg ggc cag ctg aat gtg aag aat gag gag ctg gag 248
Val Leu Ala Ser Met Gly Gln Leu Asn Val Lys Asn Glu Glu Leu Glu
      55   60   65

gcc atg atc aag gaa gcc agc ggc cca atc aac ttc acc gtt ttc ctc 296
Ala Met Ile Lys Glu Ala Ser Gly Pro Ile Asn Phe Thr Val Phe Leu
  70   75   80   85

acc atg ttc gga gag aag ttg aag ggt gct gac ccc gaa gac gtc atc 344
Thr Met Phe Gly Glu Lys Leu Lys Gly Ala Asp Pro Glu Asp Val Ile

```
gtg tct gcc ttc aag gtg ctg gac cct gag ggc act gga tcc atc aag    392
Val Ser Ala Phe Lys Val Leu Asp Pro Glu Gly Thr Gly Ser Ile Lys
            105                 110                 115

aag gaa ttc ctt gag gag ctt ttg acc act cag tgc gac agg ttc acc    440
Lys Glu Phe Leu Glu Glu Leu Leu Thr Thr Gln Cys Asp Arg Phe Thr
            120                 125                 130

gca gag gag atg aag aat ctg tgg gcc gcc ttc ccc cca gat gtg gct    488
Ala Glu Glu Met Lys Asn Leu Trp Ala Ala Phe Pro Pro Asp Val Ala
            135                 140                 145

ggc aat gtt gac tac aag aac atc tgc tac gtc atc aca cac gga gag    536
Gly Asn Val Asp Tyr Lys Asn Ile Cys Tyr Val Ile Thr His Gly Glu
150                 155                 160                 165

gag aag gag gag taa acaaccttgg aatagaggaa cgaagagaa gaacatgcat    591
Glu Lys Glu Glu
            170

cctcacagct taatctccag tctgttgtct ggccttctct aacttttgtt tttccttcct 651

ccctttcttg ctttctacca tcgttgttac tccaagcact tacactctcc atcttaccaa 711

agacttgtct cgctgggact gaattgggag ggtggagagg aacacgacca cagtgtctgt 771

cgagtgggga catgggattg ttttcaataa aatgaacatc atttctgtat ctctcacatt 831

ctctctttct ctctgtttct cactcattac ccacaacccc tctctttcat ttcagtcaag 891

cttgcatgta agtcgctgct tcttctgctg cagtcttagg agttgaaacg aaggcatcta 951

tagtttgggg ctgaaacatc tctctagatc aatgtggaag agtgctcact ctgaggggga 1011

aagaagcacg atggagtgat ctcactctat aatagaggaa ccagtcatca ttctcatttc 1071

ctcctctggt ggttgactaa aaagagaaag agaaatgag ggttttgtgc tgagtgagtt 1131

tagcctccta aaagcgatgc cgagctcatc acagagggag tgagagggac agaccatcct 1191

aggaagagag gagagcaggg actgaaagaa aacataacct cttcactccc cctctcccct 1251

cctcttctct atttctctgt ccatcttttc ttttttcttt tttctttttt gctttctgca 1311

tctgggcctg ctttgctctg ccaaacctct cctgtaacca ataaaaagac acaaactgtg 1371

aataaaaaaa aaaaaaaaaa a                                           1392
```

<400> 21

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Met Ala Pro Lys Lys Ala Lys Arg Arg Ala Ala Gly Gly Glu Gly Ser
1               5                   10                  15
Ser Asn Val Phe Ser Met Phe Glu Gln Ser Gln Ile Gln Glu Tyr Lys
            20                  25                  30
Glu Ala Phe Thr Ile Ile Asp Gln Asn Arg Asp Gly Ile Ile Ser Lys
        35                  40                  45
Asp Asp Leu Arg Asp Val Leu Ala Ser Met Gly Gln Leu Asn Val Lys
    50                  55                  60
Asn Glu Glu Leu Glu Ala Met Ile Lys Glu Ala Ser Gly Pro Ile Asn
65                  70                  75                  80
Phe Thr Val Phe Leu Thr Met Phe Gly Glu Lys Leu Lys Gly Ala Asp
                85                  90                  95
Pro Glu Asp Val Ile Val Ser Ala Phe Lys Val Leu Asp Pro Glu Gly
            100                 105                 110
Thr Gly Ser Ile Lys Lys Glu Phe Leu Glu Glu Leu Leu Thr Thr Gln
            115                 120                 125
Cys Asp Arg Phe Thr Ala Glu Glu Met Lys Asn Leu Trp Ala Ala Phe
    130                 135                 140
Pro Pro Asp Val Ala Gly Asn Val Asp Tyr Lys Asn Ile Cys Tyr Val
145                 150                 155                 160
Ile Thr His Gly Glu Glu Lys Glu Glu
                165
```

<210> 22
<211> 2054
<212> DNA
<213> Danio rerio

<220>
<221> TATA signal
<222> (1983)..(1989)

<220>
<221> enhancer
<222> (142)..(148)
<223> E-box, canntg

<220>
<221> enhancer
<222> (452)..(457)
<223> E-box, canntg

<220>
<221> enhancer
<222> (1095)..(1100)
<223> E-box, canntg

<220>
<221> enhancer
<222> (1278)..(1283)
<223> E-box, canntg

<220>
<221> enhancer
<222> (1362)..(1367)

<223> E-box, canntg

<220>
<221> enhancer
<222> (1385)..(1390)
<223> E-box, canntg

<220>
<221> enhancer
<222> (523)..(532)
<223> Potential MEF2 binding site, yta(w)4tar

<220>
<221> enhancer
<222> (606)..(615)
<223> Potential MEF2 binding site, yta(w)4tar

<220>
<221> enhancer
<222> (697)..(706)
<223> Potential MEF2 binding site, yta(w)4tar

<220>
<221> enhancer
<222> (1490)..(1499)
<223> Potential MEF2 binding site, yta(w)4tar

<220>
<221> enhancer
<222> (1640)..(1649)
<223> Potential MEF2 binding site, yta(w)4tar

<220>
<221> enhancer
<222> (1956)..(1965)
<223> Potential MEF2 binding site, yta(w)4tar

<220>
<223> Transcription start site at residue 2012

<220>
<221> primer bind
<222> (2032)..(2054)
<223> M2

<220>
<221> misc difference
<222> (2027)..(2054)
<223> Identical to the 5' MLC2f cDNA

<400> 22
tgcatgcctg gcaggtccac tctagaggac tactagtcat atgcgattct gaacaatgct 60
ggaatgagcc accaactcat ccagtgtatt accctacact gggaaacacc caaatctgtc 120
tgttatattt gtgcatatac attagattag aagctgtcac tgcggtggta ccttttcaaa 180
ttgatacctc aaaagtatat attagtgcct tttaggtact aatatatacc cttgaggttt 240
tcatttggaa aggtaccacc ccagtgacag aaatctggag cttatttaac aaaataactt 300
tatttatatg ttattgaaaa atattaaata agcaaaacaa tggaaaaaaa ttagttcaaa 360

```
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